Amendments to the Claims

1. (Currently amended) A computer system for identifying a drug discovery target, the system comprising:

a computer system comprising a database to store and access genomics information wherein said genomics information is stored as an ontology; wherein:

(a) the computer system is configured to:

~~(a)~~ i) perform computational analysis of biological relationships among the stored genomics information,

~~(b)~~ ii) query the database to identify disease-related pathways; and,

~~(c)~~ iii) identify the biological objects and processes that act on those objects in the disease-related pathways whereby each object or process involved in the disease-related pathways is a drug discovery target;

(b) the genomics information comprises information relating to genes, their DNA sequences, their mRNA, proteins expressed from said genes and the biological effects of the expressed proteins, and;

(c) the ontology is organized so that:

(i) each gene, mRNA, protein expressed from said gene, and biological effect is given an identifier which is related to synonyms for the identifier;

(ii) each gene, mRNA, protein expressed from said gene, and biological effect is categorized by class; and

(iii) the relationship of each gene, mRNA, protein expressed from said gene and disease state is defined by slots and facets.

2. (Cancelled)

3. (Currently Amended) The computer system of claim [[2]] 1 wherein said genomics information comprises data extracted from multiple public sources.

4. (Currently Amended) The computer system of claim [[2]] 1 wherein said genomics information comprises proprietary data.

5. (Currently Amended) The computer system of claim [[2]] 1 wherein said genomics information comprises data extracted from a combination of proprietary and public data sources.

6. (Cancelled)

7. (Cancelled)

8. (Previously Presented) The computer system of claim 1 wherein drug discovery targets in the disease related pathway are prioritized based on factors that include function and complexity.

9. (Previously Presented) The computer system of claim 1 wherein drug discovery targets are prioritized based on markers for side effects and patient responsiveness.

10-12. (Cancelled)

13. (Previously Presented) The computer system of claim 1 wherein the genomics information comprises information relating to genotype and the disease-related pathway comprises a gene, mRNA or protein expressed from said gene associated with a particular genotype.

14. (Previously Presented) The computer system of claim 1 wherein the genomics information comprises the name of each gene, mRNA or protein expressed from said gene, and their biological effects, and the computer identifies relationships between genes and/or proteins expressed from said genes that are at least two steps removed from each other in a disease-related pathway.

15-61. (Cancelled)

62. (Previously Presented) The computer system of claim 1, further comprising a second database for a knowledge base of scientific findings.

63. (Previously Presented) The computer system of claim 62, wherein the knowledge base is a frame-based knowledge base.

64. (Previously Presented) The computer system of claim 1, wherein the system is further configured to compare disease-related pathways with data obtained from gene expression studies or a manually entered gene list.

65. (Previously Presented) The computer system of claim 64, wherein the gene expression studies comprise differential gene expression studies or microarray studies.

66. (Previously Presented) The computer system of claim 64, wherein the comparison of the disease-related pathways with user-defined data is made using a statistical model.

67. (Previously Presented) The computer system of claim 66, wherein the statistical model calculates the probability that overlaps between disease-related pathways and user-defined data is a random event.

68. (Previously Presented) The computer system of claim 1, wherein the identification step further comprises storing the identified biological objects and processes according to the ontology.

69. (Previously Presented) The computer system of claim 1, wherein performance of computational analysis of biological relationships among the stored genomics information comprises generating one or more subsets of genomics information.

70. (Previously Presented) The computer system of claim 69, wherein the one or more subsets of genomics information are pre-generated from the database.

71. (Previously Presented) The computer system of claim 69, wherein the one or more subsets of genomics information are generated by one of a data-driven and model-driven approach.

72. (Previously Presented) The computer system of claim 69, wherein the one or more subsets of genomics information are generated based upon information contained in the database and user supplied genomics information.

73. (Previously Presented) The computer system of claim 69, further comprising the step of providing a user-supplied set of gene expression data for identifying a particular subset of genomics information, wherein the gene expression data are selected based on one or more of expression levels derived from microarray experiments, a prior analysis algorithm, and a user's preferred gene set.

74. (Previously Presented) The computer system of claim 69, wherein the one or more subsets of genomics information are gene-centric being derived about a central gene for all genes in the database.

75. (Previously Presented) The computer system of claim 69, wherein the generation of one or more subsets of genomics information further comprises deriving one or more subsets of genomics information of related user-selected genes.

76. (Previously Presented) The computer system of claim 76, wherein the one or more subsets of genomics information are generated so as to be non-overlapping by ensuring that user-selected genes do not appear in more than a predetermined maximum threshold number of subset of genomics information.

77. (Previously Presented) The computer system of claim 76, wherein the one or more subsets of genomics information are generated so as to be based on connections between a first known drug target gene and a second drug target gene of interest.

78. (Previously Presented) A networked computer system for identifying a drug discovery target comprising:

a communication network; and

a computer system coupled to the communication network comprising a database for storing and accessing genomics information;

wherein the computer system is configured to:

(a) perform computational analysis of biological relationships among the stored genomics information;

(b) query the database to identify a disease-related pathway; and

(c) identify the biological objects and processes that act on those objects in the disease-related pathway whereby each object or process involved in the disease-related pathway is a drug discovery target.